AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

On page 1, following the title, please replace the first paragraph with the following:

--This is a Continuation of ~~co-pending~~ U.S. Patent Appln. Ser. No. 09/350/597, filed July 9, 1999, now U.S. Patent No. 6,458,535, which is a Continuation of U.S. Appln. Ser. No. 08/823,516, filed March 24, 1997, now U.S. Patent No. 5,994,069, which is a ~~which is a~~ Continuation-In-Part of U.S. Appln. Ser. No. ~~08/756,038~~, 08/759,038 filed December 2, 1996, now U.S. Patent No. 6,090,543, which is a Continuation-In-Part of U.S. Appln. Ser. No. 08/756,386, filed November 26, 1996, now U.S. Patent No. 5,985,557, which is a Continuation-In-Part of U.S. Appln. Ser. No. 08/682,853, filed July 12, 1996, now U.S. Patent No. 6,001,567, which is a Continuation-In-Part of U.S. Appln. Ser. No. 08/599,491, filed January 24, 1996, now U.S. Patent No. 5,846,717.--

On page 23, please replace the paragraph beginning on line 4 with the following:

--Figs. 1A to 1H is a comparison of the nucleotide structure of the DNAP genes isolated from *Thermus aquaticus* (SEQ ID NO:1), *Thermus flavus* (SEQ ID NO:2) and *Thermus thermophilus* (SEQ ID NO:3); the consensus sequence (SEQ ID NO:7) is shown at the top of each row.--

On page 23, please replace the paragraph beginning on line 8 with the following:

--Figs. 2A to 2C is a comparison of the amino acid sequence of the DNAP isolated from *Thermus aquaticus* (SEQ ID NO:4), *Thermus flavus* (SEQ ID NO:5), and *Thermus thermophilus* (SEQ ID NO:6); the consensus sequence (SEQ ID NO:8) is shown at the top of each row.--

On page 27, please replace the paragraph beginning on line 1 with the following:

--Figs. 42A and B ~~is the image~~ are images generated by a fluorescence imager showing the products of Invader™-directed cleavage assays run using a HCV RNA target and demonstrate the stability of RNA targets under Invader™-directed cleavage assay conditions.--

On page 28, please replace the paragraph beginning on line 13 with the following:

--Figs. 59 A-E provides an alignment of the amino acid sequences of several FEN-1 nucleases including the *Methanococcus jannaschii* FEN-1 protein (MJAFEN1.PRO), the *Pyrococcus furiosus* FEN-1 protein (PFUFEN1.PRO), the human FEN-1 protein (HUMFEN1.PRO), the mouse FEN-1 protein (MUSFEN1.PRO), the *Saccharomyces cerevisiae* YKL510 protein (YST510.PRO), the *Saccharomyces cerevisiae* RAD2 protein (YSTRAD2.PRO), the *Shizosaccharomyces pombe* RAD13 protein (SPORAD13.PRO), the human XPG protein (HUMXPG.PRO), the mouse XPG protein (MUSXPG.PRO), the *Xenopus laevis* XPG protein (XENXPG.PRO) and the *C. elegans* RAD2 protein (CELRAD2.PRO) (SEQ ID NOS:135-145, respectively); portions of the amino acid sequence of some of these proteins were not shown in order to maximize the alignment between proteins (specifically, amino acids 122 to 765 of the YSTRAD2 sequence were deleted; amino acids 122 to 746 of the SPORAD13 sequence were deleted; amino acids 122 to 757 of the HUMXPG sequence were deleted; amino acids 122 to 770 of the MUSXPG sequence were deleted; and amino acids 122 to 790 of the XENXPG sequence were deleted). The numbers to the left of each line of sequence refers to the amino acid residue number; dashes represent gaps introduced to maximize alignment.--

On page 31, please replace the paragraph beginning on line 22 with the following:

--~~Figs. 88~~ Figs. 88A and 88B ~~provides~~ provide a schematic illustrating that an uncut probe combined with a partial promoter oligo does not permit transcription while a cut probe combined with a partial promoter oligo generates a complete (but nicked) promoter which supports transcription.--